



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 123456789

**TO:** Nita M Minnifield  
**Location:** rem/3c01/3c18  
**Art Unit:** 1645  
**Friday, April 01, 2005**

**Case Serial Number:** 09/914454

**From:** Edward Hart  
**Location:** Biotech-Chem Library  
**REM-1A55**  
**Phone:** 571-272-2512

**edward.hart@uspto.gov**

### Search Notes

Examiner Minnifield,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



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GenCore version 5.1.6

GenCore - nucleic search, using sw model

Date: March 31, 2005, 17:42:45 ; Search time 1925 Seconds  
 Location: 395.473 Million cell updates/sec

Title: US-09-914-454B-1

Perfect score: 20

Sequence: 1 tccatgacgttctgcgtt 20

Scoring table: IDENTITY\_NUC

Gapext 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19332134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

**Database :**

- EST:\*
  - 1: gb\_est1:\*
  - 2: gb\_est2:\*
  - 3: gb\_htc:\*
  - 4: gb\_est3:\*
  - 5: gb\_est4:\*
  - 6: gb\_est5:\*
  - 7: gb\_est6:\*
  - 8: gb\_gss1:\*
  - 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result

No. Score Query Match Length DB ID

Description

#### ALIGNMENTS

**RESULT 1**  
 CI978668/c  
**DEFINITION** OsIFCC03298 Oryza Sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.  
**ACCESSION** CI978668  
**VERSION** CI978668.1 GI:52411839  
**KEYWORDS** GSS.  
**SOURCE** Oryza Sativa (indica cultivar-group)  
**ORGANISM** Oryza sativa (indica cultivar-group)  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrartoideae; Oryzeae; Oryza;  
**REFERENCE** 1 (bases 1 to 498)  
**AUTHORS** Ma,L., Wang,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.  
**TITLE** An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis  
**JOURNAL** Unpublished (2004)  
**COMMENT** Contact: Chen Chen  
 Department of Bioinformatic  
 Beijing Institute of Genomics  
 Chinese Academy of Sciences, Beijing 101300, China  
 Tel: +86-10-80481559  
 Fax: +86-10-80488676  
 Email: chencheng@genomics.org.cn  
 Rice genomic sequence.

**FEATURES**  
 source  
 /organism="Oryza sativa (indica cultivar-group)"  
 /db\_xref="taxon:3946"  
 /clone\_lib="Oryza sativa Express Library"  
 /note="Oryza sativa exon trapped genomic sequences"  
 ORIGIN  
 1. .498  
 1. Location/Qualifiers  
 /organism="Oryza sativa (indica cultivar-group)"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3946"  
 /clone\_lib="Oryza sativa Express Library"  
 /note="Oryza sativa exon trapped genomic sequences"  
 Query Match Best Local Similarity 100.0%; Pred. No. 37; Length 498;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qry** 1 TCCATGAGCTTCAGCTT 20  
**Db** 83 TCCATGAGCTTCAGCTT 64

**Database :**

- EST:\*
  - 1: CL978668
  - 2: CL978665
  - 3: CL978665 OSIFCC032
  - 4: CL978665 OSIFCC032 CC9709713 OSUBY21TV
  - 5: CL978668 000601AEP
  - 6: CL970339 OSIFCC041 CD505499 CD74\_A09
  - 7: CL95273 OSIFCC012 CI965273 OSIFCC012
  - 8: CL95273 OSIFCC012 BF713668 ESTPBL23
  - 9: CL95273 OSIFCC012 CG260054 OG2CK84TV
  - 10: CL95273 OSIFCC012 AA171941 FP24F01.9
  - 11: CL95273 OSIFCC012 AA171941 FP24F01.9
  - 12: CL95273 OSIFCC012 CL17955 104\_383\_1
  - 13: CL95273 OSIFCC012 CL17955 BR156008 RCO\_H7075
  - 14: CL95273 OSIFCC012 AW055908 697002008
  - 15: CL95273 OSIFCC012 CA158051 SCBRZ2305
  - 16: CL95273 OSIFCC012 CA11344 SCGB1B03
  - 17: CL95273 OSIFCC012 CA10903 SCURH106
  - 18: CL95273 OSIFCC012 CA15304 SCYPR2203
  - 19: CL95273 OSIFCC012 CA264770 SCAGR104
  - 20: CL95273 OSIFCC012 CA18213 SCBSG1311
  - 21: CL95273 OSIFCC012 BU253412 603412072
  - 22: CL95273 OSIFCC012 CV181077 ta168c11.
  - 23: CL95273 OSIFCC012 CCI1044 NLJ\_76114
  - 24: CL95273 OSIFCC012 CG334334 OGWR007
  - 9: CL95273 OSIFCC012 AL205647 Tetradon

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**ON Nucleic - nucleic search, using BW model**

**Run On:** March 31, 2005, 17:00:28 ; Search time 312 Seconds  
 (without alignments)  
 387,980 Million cell updates/sec

**Time:** US-09-914-454B-1  
**Prefect score:** 20  
**Sequence:** tccatgacgttctgacggtt 20

**Scoring table:** IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5607317 seqs, 3026245999 residues

Total number of hits satisfying chosen parameters:  
 Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

**Post-processing:** Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

**Database :**

Published Applications NA: \*

- 1: /cggn2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq: \*
- 2: /cggn2\_6/prodata/1/pubpna/PCT\_NEW\_PUB.seq: \*
- 3: /cggn2\_6/prodata/1/pubpna/US06\_NEW\_PUB.seq: \*
- 4: /cggn2\_6/prodata/1/pubpna/US06\_PUBCOMB.seq: \*
- 5: /cggn2\_6/prodata/1/pubpna/US07\_NEW\_PUB.seq: \*
- 6: /cggn2\_6/prodata/1/pubpna/PCTC\_PUBCOMB.seq: \*
- 7: /cggn2\_6/prodata/1/pubpna/US08\_NEW\_PUB.seq: \*
- 8: /cggn2\_6/prodata/1/pubpna/US09A\_PUBCOMB.seq: \*
- 9: /cggn2\_6/prodata/1/pubpna/US09B\_PUBCOMB.seq: \*
- 10: /cggn2\_6/prodata/1/pubpna/US09C\_PUBCOMB.seq: \*
- 11: /cggn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq: \*
- 12: /cggn2\_6/prodata/1/pubpna/US09\_NEW\_PUB.seq: \*
- 13: /cggn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq: \*
- 14: /cggn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq: \*
- 15: /cggn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq: \*
- 16: /cggn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq: \*
- 17: /cggn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq: \*
- 18: /cggn2\_6/prodata/1/pubpna/US10\_NEW\_PUB.seq: \*
- 19: /cggn2\_6/prodata/1/pubpna/US11\_PUB.seq: \*
- 20: /cggn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq: \*
- 21: /cggn2\_6/prodata/1/pubpna/US60\_NEW\_PUBCOMB.seq: \*
- 22: /cggn2\_6/prodata/1/pubpna/US60\_PUBCOMB.seq: \*

**RESULT 1**  
 Sequence 3 Application US/09760506  
 Publication No. US20010034330A1  
 GENERAL INFORMATION:  
 APPLICANT: Kemil, Charlotte  
 TITLE OF INVENTION: Imate Immunity-Stimulating Compositions of CpG and  
 FILE REFERENCE: 8449-153-999  
 CURRENT APPLICATION NUMBER: US/09/760,506  
 CURRENT FILING DATE: 2002-01-12  
 PRIOR APPLICATION NUMBER: 60/120,853  
 PRIOR FILING DATE: 2000-05-01  
 PRIOR APPLICATION NUMBER: 60/175,840  
 PRIOR FILING DATE: 2000-01-13  
 PRIOR APPLICATION NUMBER: 60/128,608  
 PRIOR FILING DATE: 1999-04-08  
 PRIOR APPLICATION NUMBER: 60/095,913  
 PRIOR FILING DATE: 1998-08-10  
 NUMBER OF SEQ ID NOS: 6

**ALIGNMENTS**

Result No.	Score	Query Match Length	DB ID	Description
1	20	100.0	20 9 US-09-760-506-3	Sequence 3, Appli
2	20	100.0	20 9 US-09-768-012-3	Sequence 3, Appli
3	20	100.0	20 9 US-09-824-468-100	Sequence 100, Appli
4	20	100.0	20 9 US-09-824-468-105	Sequence 105, Appli
5	20	100.0	20 9 US-09-949-194-1	Sequence 1, Appli
6	20	100.0	20 9 US-09-917-222-1	Sequence 1, Appli
7	20	100.0	20 9 US-09-800-266A-86	Sequence 86, Appli
8	20	100.0	20 9 US-09-800-266A-90	Sequence 90, Appli
9	20	100.0	20 9 US-09-895-007A-86	Sequence 90, Appli
10	20	100.0	20 9 US-09-895-007A-90	Sequence 86, Appli
11	20	100.0	20 9 US-09-920-313-86	Sequence 86, Appli

**SUMMARIES**

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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### Oligonucleic - nucleic search, using sw model

Run on: March 31, 2005, 16:07:48 ; Search time 95 Seconds  
(without alignments)  
344.479 Million cell updates/sec

Title: US-09-914-454B-1  
Perfect score: 20

Sequence: 1 tcacggacgttccgtgacgtt 20

Scoring table: IDENTITY\_NUC  
Gpop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:

1: /cggn2\_6/ptodata/1/ina/5A\_COMB.seq: \*  
2: /cggn2\_6/ptodata/1/ina/5B\_COMB.seq: \*  
3: /cggn2\_6/ptodata/1/ina/6A\_COMB.seq: \*  
4: /cggn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cggn2\_6/ptodata/1/ina/PCTUS\_COMB.seq: \*  
6: /cggn2\_6/ptodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	20	100.0	20	US-09-133-774-12
2	20	100.0	20	US-09-303-862-12
3	20	100.0	20	US-09-738-652-10
4	20	100.0	20	US-09-030-701-62
5	20	100.0	20	US-09-286-058-100
6	20	100.0	20	US-09-286-058-105
7	20	100.0	20	US-09-960-774-10
8	20	100.0	20	US-09-082-649B-51
9	20	100.0	20	US-09-082-649B-51
10	20	100.0	20	US-09-082-649B-58
11	20	100.0	20	US-09-325-153A-86
12	20	100.0	20	US-09-325-153A-90
13	20	100.0	20	US-09-191-170-97
14	20	100.0	20	US-09-690-911-1
15	20	100.0	20	US-09-001-839A-1
16	20	100.0	20	US-09-992-170C-42
17	20	100.0	20	US-09-337-659-10
18	20	100.0	20	US-10-405-231A-42
19	20	100.0	20	US-10-238-607-42
20	20	100.0	20	US-09-984-865-42
21	20	100.0	20	US-09-565-906-1
22	20	100.0	20	US-09-257-188A-2
23	20	100.0	20	US-09-965-101-51
24	20	100.0	20	US-09-965-101-56
25	20	100.0	20	US-09-965-101-58
26	20	100.0	44	US-09-082-649B-12
27	20	100.0	44	US-09-082-649B-13

### ALIGNMENTS

RESULT	US-09-133-774-12
SEQUENCE	Sequence 12, Appl
PATENT NO.	Patent No. 562636
GENERAL INFORMATION:	
APPLICANT:	Bachmair, Kurt
APPLICANT:	Hessel, Andrew J.
APPLICANT:	Neu M.D., Nikolaus
APPLICANT:	Penninger, Josef M.
TITLE OF INVENTION:	No. 562636el Peptides Capable of Modulating Inflammatory Heart Disease
FILE REFERENCE:	A-536
CURRENT APPLICATION NUMBER:	US/09/133,774B
CURRENT FILING DATE:	1998-08-12
NUMBER OF SEQ ID NOS:	26
SEQ ID NO:	12
LENGTH:	20
TYPE:	DNA
ORGANISM:	Chlamydia trachomatis
FEATURE:	
OTHER INFORMATION:	An oligonucleotide derived from the DNA encoding a 60 kDa cytosine rich outer membrane protein from Chlamydia trachomatis.
OTHER INFORMATION:	US-09-133-774-12
QUERY MATCH:	100.0%; Score 20; DB 2; Length 20;
BEST LOCAL SIMILARITY:	100.0%; Pred. No. 0.8; 0; Mismatches 0; Indels 0; Gaps 0;
MATCHES:	20; Conservative 0;
QY	1 TCCATGACGTTCCTGACGTT 20
DB	1 TCCATGACGTTCCTGACGTT 20
1	Sequence 1, Appl
2	Sequence 2, Appl
3	Sequence 10, Appl
4	Sequence 42, Appl
5	Sequence 42, Appl
6	Sequence 42, Appl
7	Sequence 42, Appl
8	Sequence 42, Appl
9	Sequence 97, Appl
10	Sequence 1, Appl
11	Sequence 1, Appl
12	Sequence 12, Appl
13	Sequence 1, Appl
14	Sequence 1, Appl
15	Sequence 1, Appl
16	Sequence 1, Appl
17	Sequence 1, Appl
18	Sequence 1, Appl
19	Sequence 1, Appl
20	Sequence 1, Appl
21	Sequence 1, Appl
22	Sequence 1, Appl
23	Sequence 1, Appl
24	Sequence 1, Appl
25	Sequence 1, Appl
26	Sequence 1, Appl
27	Sequence 1, Appl
28	Sequence 1, Appl
29	Sequence 1, Appl
30	Sequence 1, Appl
31	Sequence 1, Appl
32	Sequence 1, Appl
33	Sequence 1, Appl
34	Sequence 1, Appl
35	Sequence 1, Appl
36	Sequence 1, Appl
37	Sequence 1, Appl
38	Sequence 1, Appl
39	Sequence 1, Appl
40	Sequence 1, Appl
41	Sequence 1, Appl
42	Sequence 1, Appl
43	Sequence 1, Appl
44	Sequence 1, Appl
45	Sequence 1, Appl

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GenCore version 5.1.6

(c) nucleic acid search, using SW model

Run On: March 31, 2005, 17:02:04 ; Search time 1533 Seconds

632.162 Million cell updates/sec

Project Score: 20

Sequence: 1 tccatgacgttcttgacgtt 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenBank:  
 1: gb\_ba:  
 2: gb\_hg:  
 3: gb\_in:  
 4: gb\_om:  
 5: gb\_ov:  
 6: gb\_pnt:  
 7: gb\_ph:  
 8: gb\_pl:  
 9: gb\_pr:  
 10: gb\_to:  
 11: gb\_sts:  
 12: gb\_sy:  
 13: gb\_un:  
 14: gb\_vl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Blt No.	Score	Query Match Length	DB ID	Description
1	20	100.0	20	AR078395
2	20	100.0	20	AR140451
3	20	100.0	20	AR146388
4	20	100.0	20	AR146393
5	20	100.0	20	AR154681
6	20	100.0	20	BD190417
7	20	100.0	20	BD205610
8	20	100.0	20	BD205615
9	20	100.0	20	BD22610
10	20	100.0	20	BD22615
11	20	100.0	20	BD261152
12	20	100.0	20	BD261157
13	20	100.0	20	BD261307
14	20	100.0	20	BD261311
15	20	100.0	20	BD261560
16	20	100.0	20	BD267913
17	20	100.0	20	BD270813
18	20	100.0	20	BD270817
19	20	100.0	20	CQ753470

RESULTS

Query	Match	Length	DB ID	Description
1	100.0%	20	AR078395	Sequence AR078395 from patent US 5962636.
2	100.0%	20	AR140451	Sequence AR140451.1 GI:10005141
3	100.0%	20	AR146388	Sequence AR146388
4	100.0%	20	AR146393	Sequence AR146393
5	100.0%	20	AR154681	Sequence AR154681
6	100.0%	20	BD190417	Method of BD190417
7	100.0%	20	BD205610	Method of BD205610
8	100.0%	20	BD205615	Method of BD205615
9	100.0%	20	BD22610	Composite BD22610
10	100.0%	20	BD22615	Enhanceme BD22615
11	100.0%	20	BD261152	Methods a BD261152
12	100.0%	20	BD261157	Methods a BD261157
13	100.0%	20	BD261307	Methods a BD261307
14	100.0%	20	BD261311	Methods a BD261311
15	100.0%	20	BD261560	Vaccine. BD261560
16	100.0%	20	BD267913	Methods f BD267913
17	100.0%	20	BD270813	Stereoiso BD270813
18	100.0%	20	BD270817	Stereoiso BD270817
19	100.0%	20	CQ753470	Sequence CQ753470

ALIGMENTS

Query	Match	Length	DB ID	Description
1	100.0%	20	AR078395	Sequence AR078395 from patent US 5962636.
2	100.0%	20	AR140451	Sequence AR140451.1 GI:10005141
3	100.0%	20	AR146388	Sequence AR146388
4	100.0%	20	AR146393	Sequence AR146393
5	100.0%	20	AR154681	Sequence AR154681
6	100.0%	20	BD190417	Method of BD190417
7	100.0%	20	BD205610	Method of BD205610
8	100.0%	20	BD205615	Method of BD205615
9	100.0%	20	BD22610	Composite BD22610
10	100.0%	20	BD22615	Enhanceme BD22615
11	100.0%	20	BD261152	Methods a BD261152
12	100.0%	20	BD261157	Methods a BD261157
13	100.0%	20	BD261307	Methods a BD261307
14	100.0%	20	BD261311	Methods a BD261311
15	100.0%	20	BD261560	Vaccine. BD261560
16	100.0%	20	BD267913	Methods f BD267913
17	100.0%	20	BD270813	Stereoiso BD270813
18	100.0%	20	BD270817	Stereoiso BD270817
19	100.0%	20	CQ753470	Sequence CQ753470

ORIGIN

Query	Match	Length	DB ID	Description
1	100.0%	20	AR078395	Sequence AR078395 from patent US 5962636.
2	100.0%	20	AR140451	Sequence AR140451.1 GI:10005141
3	100.0%	20	AR146388	Sequence AR146388
4	100.0%	20	AR146393	Sequence AR146393
5	100.0%	20	AR154681	Sequence AR154681
6	100.0%	20	BD190417	Method of BD190417
7	100.0%	20	BD205610	Method of BD205610
8	100.0%	20	BD205615	Method of BD205615
9	100.0%	20	BD22610	Composite BD22610
10	100.0%	20	BD22615	Enhanceme BD22615
11	100.0%	20	BD261152	Methods a BD261152
12	100.0%	20	BD261157	Methods a BD261157
13	100.0%	20	BD261307	Methods a BD261307
14	100.0%	20	BD261311	Methods a BD261311
15	100.0%	20	BD261560	Vaccine. BD261560
16	100.0%	20	BD267913	Methods f BD267913
17	100.0%	20	BD270813	Stereoiso BD270813
18	100.0%	20	BD270817	Stereoiso BD270817
19	100.0%	20	CQ753470	Sequence CQ753470

DEFINITION

Query	Match	Length	DB ID	Description
1	TCCATGACGTTCCTGACGTT	20		Sequence 10 from patent US 5962636.
2	TCCATGACGTTCCTGACGTT	20		Sequence 10 from patent US 5962636.

ACCESSION

Query	Match	Length	DB ID	Description
1	TCCATGACGTTCCTGACGTT	20		Sequence 10 from patent US 5962636.

VERSION

Query	Match	Length	DB ID	Description
1	AR140451.1	20		Sequence 10 from patent US 5962636.

KEYWORDS

Query	Match	Length	DB ID	Description
1	Peptides capable of modulating inflammatory heart disease	20		Patent: US 5962636-A 12-05-OCT-1999; Location/Qualifiers

SOURCE

Query	Match	Length	DB ID	Description
1	/organism="unknown"	20		/mol_type="unassigned DNA"

Gencore Version 5.1.6  
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**On Nucleic acid search, using: sw model**

**Run On:** March 31, 2005; 16:54:48 ; Search time 255 Seconds

(without alignments) 464,293 Million cell updates/sec

**Target:** US-09-914-454B-1

**RefSeq Score:** 20

**Sequence:** tccatggacgttcctgacggtt 20

**Scoring table:** IDENTITY\_NUC

**Gapop:** 10.0 , Gapext 1.0

**Searched:** 4390206 seqs, 2959870667 residues

**Total number of hits satisfying chosen parameters:** 8780412

**Minimum DB seq length:** 0

**Maximum DB seq length:** 2000000000

**Post-processing:** Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

**Database :**  
N\_Geneseq\_16dec04,\*  
1: geneseqn1980s;\*  
2: geneseqn1990s;\*  
3: geneseqn2000s;\*  
4: geneseqn2001aa;\*  
5: geneseqn2001ba;\*  
6: geneseqn2002aa;\*  
7: geneseqn2002ba;\*  
8: geneseqn2003aa;\*  
9: geneseqn2003ba;\*  
10: geneseqn2003bb;\*  
11: geneseqn2004aa;\*  
12: geneseqn2004ba;\*  
13: geneseqn2004bb;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result	No.	Score	Query Match Length	DB ID	Description
RESULT 1	1	20	100.0	2 AAV60950	Aav60950 Unmethylated cytosine-guanine dinucleotide containing oligonucleotide 1.
	2	20	100.0	2 AAV47683	Aav47683 Unmethylated cytosine-guanine dinucleotide containing oligonucleotide 1.
	3	20	100.0	2 AAV22667	Aav27567 Immuno-stimulatory sequence
	4	20	100.0	2 AZA1946	Aaz41946 IL-12 sec
	5	20	100.0	2 AZA1949	Aaz41949 IL-12 sec
	6	20	100.0	2 AAX78802	Aax78802 HPV fusion protein
	7	20	100.0	2 AZZ1943	Aaz31943 CpG adjuvant
	8	20	100.0	2 AAV4237	Aav74237 CpG-N motif
	9	20	100.0	2 AAV7244	Aav74244 CpG-N motif
	10	20	100.0	2 AAV74242	Aav74242 CpG-N motif
	11	20	100.0	2 AAX88536	Aax88536 Cytosine-guanine dinucleotide
	12	20	100.0	2 AZZ2191	Aaz28191 Chlamydia trachomatis
	13	20	100.0	2 AZZ61012	Aaz61012 Nucleoid
	14	20	100.0	2 AZZ61010	Aaz61010 Nucleoid
	15	20	100.0	3 AZZ8025	Aaz48025 Immune response
	16	20	100.0	3 AZZ8022	Aaz48022 Immune response
	17	20	100.0	3 AZZ7885	Aaz47885 Immuno-stimulatory sequence
	18	20	100.0	3 AZA7887	Aaz47887 Immuno-stimulatory sequence
	19	20	100.0	3 AZA0447	Aaz40447 CpG adjuvant
	20	100.0	3 AZZ99174	Aaz99174 Inflammatory	

**ALIGMENTS**

21	20	100.0	20	3 AAZ99004	Aaz99004 CpG motif
22	20	100.0	20	3 AAZ4601	Aaz4601 Murine immunostimulatory sequence
23	20	100.0	20	3 AAC62277	Aac62277 Immunostimulatory sequence
24	20	100.0	20	3 AAC64136	Aac64136 Immunostimulatory sequence
25	20	100.0	20	4 AAH20390	Aah20390 CpG motif
26	20	100.0	20	4 AAC82106	Aac82106 Oligonucleotide
27	20	100.0	20	4 AAH50580	Aah50580 CpG motif
28	20	100.0	20	4 AAH1260	Aah1260 CpG oligo
29	20	100.0	20	4 AAF9805	Aaf9805 CpG immunostimulatory sequence
30	20	100.0	20	4 AAF5506	Aaf5506 Immunostimulatory sequence
31	20	100.0	20	4 AAF95501	Aaf95501 Immunostimulatory sequence
32	20	100.0	20	4 AAF9752	Aaf9752 Immunostimulatory sequence
33	20	100.0	20	4 AAF9748	Aaf9748 Immunostimulatory sequence
34	20	100.0	20	4 AAF9745	Aaf9745 Immunostimulatory sequence
35	20	100.0	20	4 AAF9544	Aaf9544 Immunostimulatory sequence
36	20	100.0	20	4 AAF93752	Aaf93752 Immunostimulatory sequence
37	20	100.0	20	4 AAF9315	Aaf9315 Immunostimulatory sequence
38	20	100.0	20	4 AAF9750	Aaf9750 Immunostimulatory sequence
39	20	100.0	20	4 AAF9744	Aaf9744 Immunostimulatory sequence
40	20	100.0	20	4 AAF9751	Aaf9751 Immunostimulatory sequence
41	20	100.0	20	4 AAF9012	Aaf9012 Immunostimulatory sequence
42	20	100.0	20	4 AAF93746	Aaf93746 Immunostimulatory sequence
43	20	100.0	20	4 AAF93753	Aaf93753 Immunostimulatory sequence
44	20	100.0	20	4 AAF9817	Aaf9817 Immunostimulatory sequence
45	20	100.0	20	4 AAF99749	Aaf99749 Immunostimulatory sequence

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result	No.	Score	Query Match Length	DB ID	Description
RESULT 1	1	20	100.0	1 AAV60950	Aav60950 standard; DNA; 20 BP.
	2	20	100.0	1 AAV60950	Aav60950 standard; DNA; 20 BP.
	3	20	100.0	1 AAV60950	Aav60950 standard; DNA; 20 BP.
	4	20	100.0	1 AAV60950	Aav60950 standard; DNA; 20 BP.
	5	20	100.0	1 AAV60950	Aav60950 standard; DNA; 20 BP.
	6	20	100.0	1 AAV60950	Aav60950 standard; DNA; 20 BP.
	7	20	100.0	1 AAV60950	Aav60950 standard; DNA; 20 BP.
	8	20	100.0	1 AAV60950	Aav60950 standard; DNA; 20 BP.
	9	20	100.0	1 AAV60950	Aav60950 standard; DNA; 20 BP.
	10	20	100.0	1 AAV60950	Aav60950 standard; DNA; 20 BP.
	11	20	100.0	1 AAV60950	Aav60950 standard; DNA; 20 BP.
	12	20	100.0	1 AAV60950	Aav60950 standard; DNA; 20 BP.
	13	20	100.0	1 AAV60950	Aav60950 standard; DNA; 20 BP.
	14	20	100.0	1 AAV60950	Aav60950 standard; DNA; 20 BP.
	15	20	100.0	1 AAV60950	Aav60950 standard; DNA; 20 BP.
	16	20	100.0	1 AAV60950	Aav60950 standard; DNA; 20 BP.
	17	20	100.0	1 AAV60950	Aav60950 standard; DNA; 20 BP.
	18	20	100.0	1 AAV60950	Aav60950 standard; DNA; 20 BP.
	19	20	100.0	1 AAV60950	Aav60950 standard; DNA; 20 BP.
	20	100.0	1 AAV60950	Aav60950 standard; DNA; 20 BP.	

**ALIGMENTS**